

RESULT 3

Y13221
 LOCUS Y13221 3686 bp DNA linear BCT 28-AUG-1997
 DEFINITION Corynebacterium glutamicum glnA gene.
 ACCESSION Y13221
 VERSION Y13221.1 GI:2342561
 KEYWORDS glnA gene; glutamine synthetase I.
 SOURCE Corynebacterium glutamicum
 ORGANISM Corynebacterium glutamicum
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 REFERENCE 1
 AUTHORS Jakoby,M., Tesch,M., Sahm,H., Kramer,R. and Burkovski,A.
 TITLE Isolation of the Corynebacterium glutamicum glnA gene encoding
 glutamine synthetase I
 JOURNAL FEMS Microbiol. Lett. 154 (1), 81-88 (1997)
 PUBMED 9297824
 REFERENCE 2 (bases 1 to 3686)
 AUTHORS Jakoby,M.J.
 TITLE Direct Submission
 JOURNAL Submitted (16-MAY-1997) M.J. Jakoby, Forschungszentrum Juelich, IBT
 I, Postfach 1913, 52428 Juelich, FRG
 FEATURES
 Location/Qualifiers
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 WWRNGKETNLDGTPNLGAKNRVKGGYFPVAPYDQTVDRVDDMVRNLAASGFALERFHH
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 APINLVYSQRNRSAAVRIPITGSNPKAKRIEFRAPDP SGNPYLGFAAMMMAGLDGIKN
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ORIGIN

Query Match 98.7%; Score 2466.4; DB 14; Length 3686;
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Qy 1 CTCTGTGCGGGGACGAAAAATTTGCAACTCTCGCTTTGTCTAGCTAGATCAACCCCAACCA 60
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 Db 401 CTCTGTGCGGGGACGAAAAATTTGCAACTCTCGCTTTGGCTAGCTAGATCAACCCCAACCA 460
 Qy 61 AGCACGAAGGGCGTCGATCCCCGCAAAGATCGGCGCCCATAAATTTCACTCAAGACAAAT 120
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 Qy 121 TACCCGCGGATAACTGCAGTTCCCGTTGCCTTGTCTGGAGCCACGGCCGTCAGCATCC 180
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Qy	181	ACCATCACGGCAGGCAGAATCAAAATGGTCAGCAGTGGACGAACCAGCGCACGCCACCAA	240
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Qy	241	CCCACACGCTCCTCTGCATCCACACGCGCAAGGCCCATGCCAAACACGGCATGACCTGGG	300
Db	641	CCCACACGTTCTCTGCATCCACACGCGCAAGGCCCATGCCAAACACGGCATGACCTGGG	700
Qy	301	GTGCGAGCAAAGATCCATCCCGTTAGCCAACCCAGGATCACGAAAATAATGAGCGTGGAT	360
Db	701	GTGCGAGCAAAGATCCAACCGTAAGCCAACCCAGGATCACGAAAATAATGAGCGTGGAT	760
Qy	361	GTCGCTACATCGCCCAGCACATCCGTGAAATTGGACAGCACAAATAGCAATAACCCAGGAA	420
Db	761	GTCGCTACATCGCCCAGCACATCCGTGAAATTGGACAGCACAAATAGCAATAACCCAGGAA	820
Qy	421	ACACCCAGTCCACGCAGACCCCGCCGATACGACGAGCCACTGAGGACAGAGAGCCGGCC	480
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Qy	481	CCTTCTTGAGGAAGCCCCAACTTTTCGCCAGGCCACCTGCCGGGCGCATCAGGATCGTCA	540
Db	881	CCTTCTTGAGGAAGCCCCAACTTTTCGCCAGGCCACCTGCCGGGTGCATCAGGATCGTCA	940
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Db	941	AAATCAGCTGGAATTTTCGGGTCCGTCAAGCCAACCTTCTCTTCGGCTTTGCCATTGTTACA	1000
Qy	601	ATCAAATCCAAACATGTAGAGGGCGGATACTGCAGTCAAAAGGCGTTGCCTTTAGACGTC	660
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Qy	721	GAAAAGTTTGTATAGATCGACAGGTAATGCATTATACTGACAACGTCGCAAGGACTACAT	780
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Db	1301	GTCAAGTTCATCAAGGATGAAAACGTCGAGTTCGTTGACGTTTCGATTACCGACCTTCCC	1360
Qy	961	GGCACCAGCAGCACTTCAGCATCCCAGCTGCCAGCTTCGATGCAGATACAGTCGAAGAA	1020
Db	1361	GGCACCAGCAGCACTTCAGCATCCCAGCTGCCAGCTTCGATGCAGATACAATCGAAGAA	1420
Qy	1021	GGTCTCGCATTCGACGGATCCTCGATCCGTGGCTTCACCACGATCGACGAATCTGACATG	1080
Db	1421	GGTCTCGCATTCGACGGATCCTCGATCCGTGGCTTCACCACGATCGACGAATCTGACATG	1480
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Db	1481	AATCTCCTGCCAGACCTCGGAACGGCCACCCTTGATCCATTCCGCAAGGCAAAGACCCTG	1540
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Db	1541	AACGTTAAGTTCTTCGTTACGATCCTTTACCCGCGAGGCATTCTCCGCGACCCACGC	1600
Qy	1201	AACGTAGCAGCAAGGCAGAGCAGTACCTGGCATCCACCGGCATTGCAGACACCTGCAAC	1260

Db	1601	AACGTGGCAGCAAGGCAGAGCAGTACCTGGCATCCACCGGCATTGCAGACACCTGCAAC	1660
Qy	1261	TTCGGCGCCGAGGCTGAGTTCTACCTCTTCGACTCCGTTGCTACTCCACCGAGATGAAC	1320
Db	1661	TTCGGCGCCGAGGCTGAGTTCTACCTCTTCGACTCCGTTGCTACTCCACCGAGATGAAC	1720
Qy	1321	TCCGGCTTCTACGAAGTAGATACCGAAGAAGGCTGGTGAACCGTGGCAAGGAAACCAAC	1380
Db	1721	TCCGGCTTCTACGAAGTAGATACCGAAGAAGGCTGGTGAACCGTGGCAAGGAAACCAAC	1780
Qy	1381	CTCGACGGAACCCCAAACCTGGGCGCAAAGAACC	1440
Db	1781	CTCGACGGAACCCCAAACCTGGGCGCAAAGAACC	1840
Qy	1441	GCACCATACGACCAAAACCGTTGACGTGCGGATGACATGGTTGCAACCTCGCAGCTTCC	1500
Db	1841	GCACCATACGACCAAAACCGTTGACGTGCGGATGACATGGTTGCAACCTCGCAGCTTCC	1900
Qy	1501	GGCTTCGCTCTTGAGCGTTTCCACCACGAAGTCGGTGGCGGACAGCAGGAAATCAACTAC	1560
Db	1901	GGCTTCGCTCTTGAGCGTTTCCACCACGAAGTCGGTGGCGGACAGCAGGAAATCAACTAC	1960
Qy	1561	CGCTTCAACACCATGCTCCACGCGGCAGATGATATCCAGACCTTCAAGTACATCATCAAG	1620
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Db	2021	AACACCGCTCGCCTCCACGGCAAGGCTGCAACCTTCATGCCTAAGCCACTGGCTGGCGAC	2080
Qy	1681	AACGGTTCCGGCATGCACGCTCACCAGTCCCTCTGGAAGGACGGCAAGCCACTCTTCCAC	1740
Db	2081	AACGGTTCCGGCATGCACGCTCACCAGTCCCTCTGGAAGGACGGCAAGCCACTCTTCCAC	2140
Qy	1741	GATGAGTCCGGCTACGCAGGCCTGTCCGACATCGCCCGCTACTACATCGGCGGCATCCTG	1800
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Qy	1801	CACCACGCAGGCGCTGTTCTGGCGTTCACCAACGCAACCCTGAACTCCTACCACCGTCTG	1860
Db	2201	CACCACGCAGGCGCTGTTCTGGCGTTCACCAACGCAACCCTGAACTCCTACCACCGTCTG	2260
Qy	1861	GTTCCAGGCTTCGAGGCTCCAATCAACCTGGTGTACTCACAGCGCAACCGTTCCGCTGCT	1920
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Qy	2161	CAGGAAGACACCGACTTCCTCACCAGTCTGACGTCTTCACCGAGGATCTCATCGAGGCG	2220
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Qy	2221	TACATCCAGTACAAGTACGACAACGAGATCTCCCCAGTTCGCCTGCGCCCAACCCCGCAG	2280
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Qy	2281	GAATTCGAATTGTACTTCGACTGCTAATTCACCTTAGCTAGCCGATAGCGGAAACCCCTG	2340

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Qy      2401 GGATCCTCCATCATGGTGGATCCGGCGCTTTTATCTATTGTTTTTGGGCTAGATGCCGA 2460
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Db      2801 GGATCCTCCATCATGGTGGATCCGGCGCTTTTATTTATTAGTTTTTGGGCTAGATGCCGA 2860
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